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Summary

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* Provides analytic support for various platforms including RNA-seq, genomics, gene expression microarrays, proteomics, metabolomics, methylation arrays, metagenomics, and metatranscriptomics
* Programs in Python, R, SQL, and Unix shell
* Interfaces and supports users with multiple servers, OSs, and HPC clusters
* Provides technical support for relational databases, servers, LIMS systems, and workstations
* Diverse background in human genetics, plant genetics, microbial metagenomics, biomedical informatics, qualitative research in public health, and HIT implementation
* Extensive experience in remote employment

**Keywords**: bioinformatics, data management, clinical research, computer programming, databases

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Education

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**Biomedical Informatics (M.S.) -**University of Utah, School of Medicine (2014)

Title:“Implementing a Personal Health record and Training Plan for the Underserved populations of the

Midvale CBC Community Clinic “

GPA:3.91

**Molecular Biology (M.S.) -** Utah State University (2013)

Title: “A Review of Apomixis and Differential Expression Analyses Using Microarrays”

GPA:3.83

**Genetics and Biotechnology (B.S.) -** Brigham Young University (2007)

Minor: Portuguese

GPA:3.51

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Work Experience

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**Research Services Principal Professional**

University of Colorado Anschutz Medical Campus / Aurora, CO | Remote / Oct 2016 – Current

* Lead and provide support for various project-driven analysis projects including RNA-seq, methylation (Illumina 450k and EPIC), gene expression microarrays (Agilent and Affymetrix), metabolomics, proteomics, eQTLs, co-localization, snRNA-seq, WGS, and other statistical modeling using R, Python, high-performance computing, Google Cloud HPC, and command-line tools
* Provide bioinformatic to diverse professionals, including principal investigators, clinicians, research coordinators, university faculty, lab technicians, medical students, graduate students, post-docs, and external research collaborators
* Implement, configure, manage, and support custom reporting solutions and large relational databases (SQL and RESTful APIs) for lab’s clinical, radiology, and imaging research databases
* Research topics includes IPF, interstitial lung disease, asthma, genetic risk of disease in human and mouse systems
* Remote employee since Sep 2020

**Bioinformaticist**

University of Nevada, Las Vegas / Remote / Aug 2020 – Feb 2022

* Provide bioinformatic support to graduate students and UNLV faculty in various project-driven analysis projects using publicly available datasets. Including RNA-seq, Hi-C, and protein sequences using Python, R, high-performance computing, and command-line tools
* Research topics included epigenomic evolution of enhancers/promoters in primates, evolution of secondary structures in proteins

**Research Assistant / Contractor**

University of Utah / Ohio State University / Remote / Nov 2013 – Dec 2020

* Remote member of evaluation team for the funded public health grants:
	+ Enhancing Utah’s All Claims and Payers Database for Healthcare Cost Transparency
	+ Utah’s State Innovation Model (SIM) Round Two Design award
* Participate in qualitative research and evaluation practices such as interviewing key informants and stakeholder groups, development of use cases, and literature research of best practices
* Assist in preparing grants and manuscripts
* Self-accountable and task oriented

**Microbial Genomics Software Engineer**

University of Hawaii at Manoa / Honolulu, HI / Apr 2015 – Aug 2016

* Provide bioinformatic and IT support to graduate students, post-docs, and research collaborators with various platforms, such as Python (including Jupyter Notebooks), Unix, Galaxy, command-line use, and interfacing with Hawaii’s high-performance cluster
* Collaborate in various projects utilizing next-gen sequencing data, such as microbial metagenomic and metatranscriptomic annotation (using RefSeq and Silva), SlipStream Galaxy pipeline development, assemblies, and comparisons of large data sets.
* Provide technical support to graduate students and post-docs for computer (Mac and PC), server (Ubuntu, Fedora, CentOS, FreeNAS), Clarity LIMS, wireless networking, and peripherals
* Taught and presented to undergraduate students the bioinformatics tool Galaxy at the 2015 CMORE Summer Course on Microbial Oceanography
* Implement, configure, and support Illumina’s (Genologics) Clarity LIMS data management platform

**Business Analyst – R&D**

Hawaii Medical Service Association / Honolulu, HI / Nov 2014 – April 2015

* Configure health plan benefits, terms, and contracts in TriZetto’s QNXT platform
* Duties also include defect resolution, user requirement gathering, database management and querying (SQL), and investigating potential new use of existing software

**Graduate Research Assistant**

Utah State University / Logan, UT / Mar 2010 – July 2013

* Field research experience in biotechnology research projects
* Manage and analyze large microarray genetic data sets using Python and R
* Collaborate utilizing various bioinformatic techniques (various Bioconductor packages, Python, command-line BLAST, RMAExpress, Gene Ontologies, etc.)
* Big data manipulation and analyses (Python, R, Bioconductor)
* Research topics included epigenetics and genetics of apomixis in small flowering plants

**Research Associate**

DuPont Pioneer / Kunia, HI / Jul 2007 – Jul 2009

* IT and informatics support for various research teams across North America
* Train and create training materials for field teams, research scientists, and field managers for data collection and data management.
* Instruct and troubleshoot for company-wide database, and other proprietary software, including *ad hoc* database reports using SQL and Oracle tools
* Windows PC workstation, wireless network, peripheral, software support

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Additional Experience

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**Publications**

1. Cardwell JH. 2013. A Review of Apomixis and Differential Expression Analyses Using Microarrays. All Graduate Plan B and other Reports.  Paper 289. http://digitalcommons.usu.edu/gradreports/289
2. Garvin JH, Cardwell JH, Doing-Harris K, Bolton D, Snow LA, Hawley CW, Xu W. 2018. Collaborative Evaluation for the Utah All Payer Claims Database Capacity Enhancement. Technology and Investment, 9, 91-108. DOI: https://doi.org/10.4236/ti.2018.92007
3. Santos-Cortez RLP, Chiong CM, Frank DN, Ryan AF, Giese APJ, Roberts TB, Daly KA, Steritz MJ, Szeremeta W, Pedro M, Pine H, Yarza TKL, Scholes MA, Llanes EGdV, Yousaf S, Friedman N, Tantoco MLC, Wine TM, Labra PJ, Benoit J, Ruiz AG, de la Cruz RAR, Greenlee C, Yousaf A, Cardwell JH, et al. 2018. FUT2 Variants Confer Susceptibility to Familial Otitis. The American Journal of Human Genetics. Nov 1;103(5):679-690. doi: 10.1016/j.ajhg.2018.09.010
4. Larson ED, Magno JPM, Steritz MJ, Llanes EGDV, Cardwell J, et al. 2019. A2ML1 and otitis media: novel variants, differential expression and relevant pathways. Human Mutation. Apr 22. doi: 10.1002/humu.23769
5. Moore C, Blumhagen RZ, Yang IV, Walts A, Powers J, Walker T, Bishop M, Russell P, Vestal B, Cardwell JH, et al. 2019. Resequencing Study Confirms That Host Defense and Cell Senescence Gene Variants Contribute to the Risk of Idiopathic Pulmonary Fibrosis.American Journal of Respiratory and Critical Care Medicine. Jul 15;200(2):199-208. doi: 10.1164/rccm.201810-1891OC
6. Qi C, Jiang Y, Yang I, Forno E, Wang T, Vonk J, Gehring U, Smit H, Milanzi E, Carpaij O, Berg M, Hesse L, Brouwer S, Cardwell J, et al. 2020. Nasal DNA methylation profiling of asthma and rhinitis. In press at The Journal of Allergy and Clinical Immunology. Jan 14; https://doi.org/10.1016/j.jaci.2019.12.911
7. Hoang T, Sikdar S, Xu CJ, Lee MK, Cardwell J, et al. 2020.  Epigenome-Wide Association Study of DNA Methylation and Adult Asthma in the Agricultural Lung Health Study. European Respiratory Journal. 2020 Sept 3;56(3):2000217
8. FurusawaH, CardwellJH, OkamotoT, et al. 2020. Chronic Hypersensitivity Pneumonitis, an Interstitial Lung Disease with Distinct Molecular Signatures. Am J Respir Crit Care Med. Nov 15;202(10):1430-1444. doi: 10.1164/rccm.202001-0134OC.
9. Mathai SK, Cardwell J, Metzger F, et al. 2020. Preclinical Pulmonary Fibrosis (PrePF) Circulating Protein Biomarkers. Am J Respir Crit Care Med. Dec 15;202(12):1720-1724. doi: 10.1164/rccm.202003-0724LE.
10. KonigsbergI, BorieR, WaltsA, CardwellJ, et al. 2021. The molecular landscape of idiopathic pulmonary fibrosis. Am J Respir Cell Mol Biol. 2021 Oct; 65(4): 430–441.
11. Gally F, Sasse S, Kurche J, Cardwell J, et al. 2021. Gain-of-function MUC5B Promoter Variant, Strongly Linked to Idiopathic Pulmonary Fibrosis, Defines an Epigenetically Poised Enhancer. JCI Insight 2021 Jan 25;6(2)
12. Konigsberg I, Borie R, Walts A, Cardwell J, et al. 2021. Molecular Signatures of Idiopathic Pulmonary Fibrosis.Am J Respir Cell Mol Biol. Oct;65(4):430-441. doi: 10.1165/rcmb.2020-0546OC.
13. Furasawa H, Peljto A, Walts AD, Cardwell J, et al. 2022. Common idiopathic pulmonary fibrosis risk variants are associated with hypersensitivity pneumonitis. Thorax. (77):508-510.
14. Borie R, Cardwell J, Konigsberg I, et al. 2022. Colocalization of gene expression and DNA methylation with genetic risk variants in MUC5B and DSP. Am J Respir Crit Care Med. Jul 11. doi: 10.1164/rccm.202110-2308OC
15. Ghosh AJ, Moll M, Hobbs BD, Cardwell J, et al. 2022. Variability in *MUC5B* expression is dependent on genotype and endotype in idiopathic pulmonary fibrosis. Under review at AJRCCM
16. Dobrinskikh E, Hennessy C, Kurche J, Kim E, Estrella A, Cardwell J, et al. 2022. Epithelial ER stress enhances the risk of Muc5b associated lung fibrosis. Under review at AJRCCM
17. Kim E, Hennessy C, Hatakka K, Huber J, Cardwell J, et al. 2022. Aberrant multiciliogenesis in idiopathic pulmonary fibrosis (IPF). Under review at AJRCMB
18. Peljto AL, Blumhagen RZ, Walts AD, Cardwell J, et al. 2022. Idiopathic pulmonary fibrosis is associated with common genetic variants and a limited number of rare variants. Under review at The Lancet Respiratory Medicine
19. Cardwell J, Kalsy M, Hand B, et al. 2022. Exploring the status of behavioral health care coordination and information exchange in the state of Utah. In preparation

**Conference Presentations**

1. Cardwell JH. Probe Masking of Arabidopsis Microarrays to Detect Differential Gene Expression in Ovules of Sexual and Apomictic *Boechera* (Brassicaceae). Oral session presented at: ASA, CSSA, and SSSA Annual Meeting 2010; Oct 31-Nov 3; Long Beach, CA.
2. Lacey JA, Pattanayak J, Jamison M, Cardwell JH, Dwivedi KK, Ulrich TH, Carman JG. Ovule Transcriptomes of Weakly Aposporous and Non-aposporous F2 Sorghum Sibs. Oral session presented at: Plant & Animal Genome XX 2012. Jan 14-18; San Diego, CA
3. Cardwell JH, Doing-Harris K, Kalsy M, Xu W, and Garvin JH. Adopting a Collaborative Program Evaluation Model to Aid Administration and Evaluation of a Large-Scale Public Health IT Grant. Poster session presented at: AMIA Annual Symposium 2014; Nov 15-19; Washington DC
4. Garvin JH, Doing-Harris K, Davis K, Cardwell JH, Hawley C, and Xu W.  Developing a Collaborative Evaluation Framework for Utah’s APCD.  Podium session presented at: AMIA 2015 Annual Symposium; Nov 14-18; San Francisco, CA
5. Yamahara KM, Preston CM, Pargett D, Jensen S, Roman B, Romano A, Cardwell J,Birch J, Delong E, Scholin C. Towards a Mobile Ecogenomic Sensor: Development and Applications of the 3rd Generation Environmental Sample Processor. Poster session presented at: DOE JGI Genomics of Energy & Environmental Meeting 2016; Mar 21-24; Walnut Creek, CA
6. Preston CM, Pargett D, Yamahara K, Jensen S, Roman B, Romano A, Cardwell J, Hobson B, Kieft B, Ryan J, Zhang Y, Birch J, DeLong E, Bellingham J, Scholin C. Sample Acquisition and Preservation on Mobile Ecogenomic Sensors in Support of Microbial Studies. Oral session presented at: ASM Microbe 2016; Jun 16-20; Boston, MA
7. Garvin JH, Doing-Harris K, Cardwell JH, Bolton D, Snow LA, Hawley CW, and Xu W. 2017. Collaborative evaluation for the Utah All Payer Claims Database capacity enhancement. Podium presentation to be presented at: International Improvement Science and Research Symposium 2017; Apr 26; London, UK
8. MathaiSK, Huber J, Cardwell JH, Yacoub M, Gaydos J, Burnham EL, Zhang Y, FingerlinTE, YangIV, SchwartzDA. Transcriptomic alterations in lung tissue and proximal airway cells associated with MUC5B gene expression are associated with cilia. Poster presented at: International Colloquium on Lung and Airway Fibrosis 2018; Oct 14-18; Pacific Grove, CA
9. MathaiSK, KropskiJA, CardwellJH, HauckS, MetzgerF, PowersJ, WaltsA, MarkinC, BrownKK, SteeleMP, SchwarzMI, LynchDA, EickelbergO, FingerlinTE, LoydJE, YangIV, SchwartzDA. Circulating plasma proteins differentially detected in Idiopathic Pulmonary Fibrosis and in subjects with Pre-Clinical Pulmonary Fibrosis. Abstract submitted to: ATS International Conference 2019; May 17-22; Dallas, TX
10. Xu C, Qi C, Forno E, Celedon J, Chen W, Nawjin MC, Cardwell JH, Yang IV, Koppelman GH. Nasal epithelial methylation in asthma. Abstract submitted to: ATS International Conference 2019; May 17-22; Dallas, TX
11. Xu C, Qi C, Forno E, Celedon J, Chen W, Nawjin MC, Cardwell JH, Yang IV, Koppelman GH. Nasal epithelial methylation in asthma. Abstract submitted to: ATS International Conference 2019; May 17-22; Dallas, TX
12. Yang IV, Cardwell J, Pulit S, Zhang W, Borie R, Walts A, Powers J, Fingerlin TE, Rojas M, Sachs N, Zappala Z, Schwartz DA. Functional validation of MUC5B and DSP Genetic Variants in Idiopathic Pulmonary Fibrosis (IPF) by Expression Quantitative Trait Locus (eQTL) and co-Localization Analyses. Abstract submitted to: ATS International Conference 2019; May 15-20; Philadelphia, PA
13. Furuswa H, Cardwell J, Cool C, Lee J, Okamoto T, Walts A, Konigsberg I, Kurche J, and Yang IV. Chronic Hypersensitivity Pneumonitis (CHP), an Interstitial Lung Disease (ILD) with Distinct Molecular Signatures. Abstract submitted to: ATS International Conference 2019; May 15-20; Philadelphia, PA
14. Konigsberg I, Borie R, Walts A, Cardwell J, Rojas M, Metzger F, Hauck S, Fingerlin TE, Yang IV, Schwartz DA. A Multi-Omic Analysis of Idiopathic Pulmonary Fibrosis. Abstract submitted to: ATS International Conference 2019; May 15-20; Philadelphia, PA
15. Matson S, Cardwell J, Yang IV, Deane K, Ryu J, Matteson E, Wolters P, Schwartz DA, Lee J. Circulating Protein Biomarkers in Rheumatoid Arthritis Associated Interstitial Lung Disease. Abstract submitted to: ATS International Conference 2019; May 15-20; Philadelphia, PA

**Other**

* Provided professional workstation support for Mac, Windows, and Linux
* Experienced in professional computer networking, workstation, peripheral, and software support
* Quick self-learner of new software and tools
* Numerous math, stats, computer programming, and bioinformatics coursework completed
* Fluent in Portuguese
* Previous on-call technician to cut up, sample, and store whole lung explants in UCHealth University Hospital pathology lab
* Eagle Scout